

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 08:31:55 ; Search time 13 Seconds
(without alignments)
79.762 Million cell updates/sec

Title: US-09-913-524-1

Perfect score: 143

Sequence: 1 PWSFSAFLRLQRPPEPAHANCHR 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	143	100.0	366	1	IHA_HUMAN	P05111	homo sapien
2	140	97.9	367	1	IHA_HORSE	P55101	equus caball
3	135	94.4	265	1	IHA_SHEEP	P38440	ovis aries
4	135	94.4	360	1	IHA_BOVIN	P07994	bos taurus
5	131	91.6	364	1	IHA_PIG	P04087	sus scrofa
6	131	91.6	366	1	IHA_MOUSE	Q04997	mus musculus
7	128	89.5	366	1	IHA_RAT	P17490	rattus norv
8	124	86.7	361	1	IHA_TRITU	Q77755	trichosurus
9	102	71.3	329	1	IHA_CHICK	P43031	gallus gall
10	55.5	38.8	368	1	GP62_HUMAN	Q9BZJ7	homo sapien
11	53	37.1	352	1	TPO_CANFA	P42705	canis fami
12	50	35.0	192	1	NIF2_FRAAL	P46040	frankia aln
13	50	35.0	528	1	DRTS_DAUCA	P45350	daucus caro
14	48.5	33.9	888	1	SM6B_HUMAN	Q9H3T3	homo sapien
15	48	33.6	606	1	HMLD_DROAN	P22544	drosophila
16	47.5	33.2	885	1	SM6B_MOUSE	Q54551	mus musculus
17	47.5	33.2	887	1	SM6B_RAT	Q70141	rattus norv
18	47	32.9	303	1	SPAO_SALDU	Q53968	salmonella
19	47	32.9	303	1	SPAO_SALTI	Q56022	salmonella
20	47	32.9	303	1	SPAO_SALTY	P40699	salmonella
21	47	32.9	442	1	BNB_DROME	P29746	drosophila
22	47	32.9	518	1	DRT2_ARATH	Q05763	arabidopsis
23	47	32.9	519	1	DRT1_ARATH	Q05762	arabidopsis
24	47	32.9	2504	1	FAS_HUMAN	P49327	homo sapien
25	46.5	32.5	627	1	GLGB_BACSU	P39118	bacillus su
26	46	32.2	834	1	PLSB_PSEAE	Q9HWX7	pseudomonas
27	46	32.2	1493	1	M3K1_MOUSE	P53349	mus musculus
28	46	32.2	1509	1	GSRI_HUMAN	Q9NMZ4	homo sapien
29	45.5	31.8	510	1	CHLE_CHLVU	P56302	chlorella v
30	45.5	31.8	646	1	PIXE_HUMAN	Q14155	homo sapien
31	45.5	31.8	646	1	PIXE_RAT	Q55043	rattus norv
32	45	31.5	95	1	VE4_HPV16	P06922	human papil
33	45	31.5	338	1	PAHX_RAT	P57093	rattus norv

RESULT 1				
ID	IHA_HUMAN	STANDARD:	PRT;	366 AA.
AC	P05111;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Inhibin alpha chain precursor.			
GN	INHA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86287350; PubMed=3016724;			
RA	Mayo K.E., Cerelli G.M., Spiess J., Rivier J., Rosenfeld M.G.,			
RA	Evans R.M., Vale W.;			
RT	"Inhibin A-subunit cDNAs from porcine ovary and human placenta.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:5849-5853(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87005283; PubMed=3758355;			
RA	Stewart A.G., Milborrow H.M., Ring J.M., Crowther C.E., Forage R.G.;			
RT	"Human inhibin genes. Genomic characterisation and sequencing.";			
RL	FEBS Lett. 206:329-334(1986).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Straussberg R.;			
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE OF 16-366 FROM N.A.			
RX	MEDLINE=86186863; PubMed=3754442;			
RA	Mason A.J., Niall H.D., Seeburg P.H.;			
RT	"Structure of two human ovarian inhibins.";			
RL	Biochem. Biophys. Res. Commun. 135:957-964(1986).			
RN	[5]			
RP	TISSUE SPECIFICITY, AND INDUCTION.			
RX	MEDLINE=98165602; PubMed=9506758;			
RA	Mellor S.L., Richards M.G., Pedersen J.S., Robertson D.M.,			
RA	Risbridger G.P.;			
RT	"Loss of the expression and localization of inhibin alpha-subunit in			
RT	high grade prostate cancer.";			
RL	J. Clin. Endocrinol. Metab. 83:969-975(1998).			
CC	!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,			
CC	RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.			
CC	INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE			
CC	FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,			
CC	GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,			
CC	ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,			
CC	EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR			
CC	SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF			
CC	ACTIVINS.			
CC	!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.			
CC	INHIBIN A IS A DIMER OF ALPHA AND BETA-A.			

P23258 homo sapien
Q92310 mus musculus
Q9nrh3 homo sapien
Q8vck3 mus musculus
P23330 xenopus lae
P54259 homo sapien
Q03696 gallus gall
Q9um47 homo sapien
Q69170 yersinia pe
Q92xp5 rhizobium m
P31361 mus musculus
P20264 homo sapien

ALIGNMENTS

CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

CC -1- TISSUE SPECIFICITY: ORIGINALLY FOUND IN OVARY (GRANULOSA CELLS)

CC AND TESTIS (SEITOLI CELLS) BUT IT IS WIDELY DISTRIBUTED IN MANY

CC TISSUES INCLUDING BRAIN AND PLACENTA. IN ADRENAL CORTEX EXPRESSION

CC IS LIMITED TO THE ZONA RETICULARIS AND THE INNERMOST ZONA

CC FASCICULATA IN THE NORMAL GLAND, EXTENDING CENTRIPETALLY INTO THE

CC ZONA FASCICULATA IN HYPERPLASIA. ALSO FOUND IN ADRENOCORTICAL

CC TUMORS. ALSO EXPRESSED IN PROSTATE EPITHELIUM OF BENIGN PROSTATIC

CC HYPERPLASIA, IN REGIONS OF BASAL CELL HYPERPLASIA AND IN

CC NONMALIGNANT REGIONS OF HIGH GRADE PROSTATE CANCER. ONLY

CC CIRCULATING INHIBIN B IS FOUND IN MALE, WHEREAS CIRCULATING

CC INHIBINS A AND B ARE FOUND IN FEMALE.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; M13981; AAA59166.1; -

CC EMBL; M13144; AAA59167.1; -

CC EMBL; BC006391; AAH06391.1; -

CC EMBL; X04445; CAA28040.1; -

CC EMBL; X04446; CAA28040.1; JOINED.

CC EMBL; A14420; CAA01158.1; -

CC PIR; A23556; A23556.

CC PIR; A24248; A24248.

CC PIR; B25947; B25947.

CC GENE; HGNC:6065; INHA.

CC MIM; 147380; -

CC InterPro: IPR002405; Inhibin_alpha.

CC InterPro: IPR001839; TGFb.

CC Pfam: PF00019; TGF-beta; 1.

CC PRINTS; PR00669; INHIBIN.

CC ProDom; PD000357; TGFb; 1.

CC SMART; SM00204; TGFb; 1.

CC PROSITE; PS00250; TGF-BETA_1; 1.

CC Growth factor; Hormone; Glycoprotein; Signal.

CC SIGNAL 1 18 POTENTIAL.

CC PROPEP 19 232

CC CHAIN 23 366 INHIBIN ALPHA CHAIN.

CC DISULFID 262 328 BY SIMILARITY.

CC DISULFID 291 363 BY SIMILARITY.

CC DISULFID 295 365 BY SIMILARITY.

CC DISULFID 327 327 INTERCHAIN (BY SIMILARITY).

CC CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).

CC CARBOHYD 268 268 N-LINKED (GLCNAC. .) (POTENTIAL).

CC CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL).

CC CONFLICT 17 17 H -> V (IN REF. 4).

CC CONFLICT 19 19 C -> S (IN REF. 4).

CC SEQUENCE 366 AA; 39669 MR; 0E03DAB12HF8E57 CRC64;

Query Match 100.0%; Score 143; DB 1; Length 366;

Best Local Similarity 100.0%; Pred. No. 2e-12;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PWSPSALRLQLQRPPEPAHANCHR 25

|||||:|||||:|||||:|||||:|||||

Db 240 PWSPSALRLQLQRPPEPAHANCHR 264

RESULT 2

THA_HORSE STANDARD; PRI: 367 AA.

AC P55101; Q28370;

DT 01-OCT-1996 (rel. 34, Created)

DT 01-OCT-1996 (rel. 34, last sequence update)

DT 16-OCT-2001 (rel. 40, last annotation update)

DE Inhibin alpha chain precursor.

GN INHA.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

ON NCBI_TaxID=9796;

RN 11

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RX MEDLINE=961559857; PubMed=8593300;

RA Yananouchi K., Yoshida S., Hasegawa T., Ikeda A., Chang K.T.,

RA Matsuyama S., Nishihara M., Miyazawa K., Takahashi M.;

RT "Molecular cloning of cDNA for inhibin alpha-subunit from equine

RT ovary".

RL J. Vet. Med. Sci. 57:905-909(1995).

RN 12

RP SEQUENCE OF 98-367 FROM N.A.

RC TISSUE=Testis;

RA Adams M.H., Baker C.B., McDowell K.J.;

RT "Molecular cloning and sequencing of equine inhibin alpha cDNA.";

RL Anim. Biotechnol. 7:11-9(1996).

CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,

CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE

CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,

CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,

CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,

CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR

CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF

CC ACTIVINS.

CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.

CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.

CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

CC -----

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CC -----

CC EMBL; D50327; BAA08863.1; -

CC EMBL; U21219; AAB00874.1; -

CC InterPro: IPR002405; Inhibin_alpha.

CC InterPro: IPR001839; TGFb.

CC Pfam: PF00019; TGF-beta; 1.

CC PRINTS; PR00669; INHIBIN.

CC ProDom; PD000357; TGFb; 1.

CC SMART; SM00204; TGFb; 1.

CC PROSITE; PS00250; TGF-BETA_1; 1.

CC Growth factor; Hormone; Glycoprotein; Signal.

CC SIGNAL 1 20 POTENTIAL.

CC PROPEP 21 233 BY SIMILARITY.

CC CHAIN 234 367 INHIBIN ALPHA CHAIN.

CC DISULFID 263 329 BY SIMILARITY.

CC DISULFID 292 364 BY SIMILARITY.

CC DISULFID 296 366 BY SIMILARITY.

CC DISULFID 328 328 INTERCHAIN (BY SIMILARITY).

CC CARBOHYD 147 147 N-LINKED (GLCNAC. .) (POTENTIAL).

CC CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).

CC CONFLICT 105 105 Q -> R (IN REF. 2).

CC CONFLICT 171 171 G -> R (IN REF. 2).

CC CONFLICT 176 176 C -> R (IN REF. 2).

CC SEQUENCE 367 AA; 39422 MR; DC8A6EB2C84B2C61 CRC64;

Query Match 97.9%; Score 140; DB 1; Length 367;

Best Local Similarity 96.0%; Pred. No. 5e-12;

Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PWSPSALRLQLQRPPEPAHANCHR 25

|||||:|||||:|||||:|||||:|||||

Db 241 PWSPSALRLQLQRPPEPAHANCHR 265

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RESULT 3
ID IHA_SHEEP STANDARD; PRT; 265 AA.
AC P38440;
DT 01-OCT-1994 (Rel. 30, Created)
DI 01-OCT-1994 (Rel. 30, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin alpha chain (Fragment).
GN INHA.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID:9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE/Ovary;
KA Sadanandan S.J., Jayaseelan K.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
CC EMBL; I26815; AAA31553.1;
CC InterPro: IPR001839; TGFb;
CC Pfam: PF000357; TGF-beta; 1.
CC ProDom: PD000357; TGFb; 1.
CC SMART: SM00204; TGFb; 1.
CC PROSITE: PS00250; TGF-BETA_1; 1.
CC Growth factor; Hormone; Glycoprotein.
CC NON_TER 1
CC DISULFID 161 227 BY SIMILARITY.
CC DISULFID 190 262 BY SIMILARITY.
CC DISULFID 194 264 BY SIMILARITY.
CC DISULFID 226 226 INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 45 45 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 167 167 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 265 AA; 28754 MW; D880E9AB156R6656 CRC64;
SQ
Query Match 94.4%; Score 135; DB 1; Length 265;
Best Local Similarity 92.0%; Pred. No. 1.7e-11;
Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 PMSPSALRLQLQRPPEPAHANCHR 25
IIII:IIII:IIII:IIII:IIII
DB 139 PMSPALELLQRPPEPAHANCHR 163
RESULT 4
ID IHA_BOVIN STANDARD; PRT; 360 AA.
AC P07594;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin alpha chain precursor.
GN INHA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE/Follicular fluid;
RX MEDLINE=86205842; PubMed=3458167;
RA Forage R.G., Rink J.M., Brown R.W., McInerney R.V., Cobon G.S.,
RA Gregson R.P., Robertson D.M., Morgan F.J., Hearn M.T.W., Findlay J.K.,
RA Wettenhall R.E.H., Burger H.G., de Kretser D.M.;
RI "Cloning and sequence analysis of cDNA species coding for the two
RI subunits of inhibin from bovine follicular fluid.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3091-3095(1986).
RN [2]
RP SEQUENCE OF 1-87 FROM N.A.
RC TISSUE-Liver;
RX MEDLINE=95112839; PubMed=7813455;
RA Thompson D.A., Cronin C.N., Martin F.;
RI "Genomic cloning and sequence analyses of the bovine alpha-, beta A-
RI and beta B-inhibin/activin genes. Identification of transcription
RI factor AP-2-binding sites in the 5'-flanking regions by DNase I
RI footprinting.";
RL Eur. J. Biochem. 226:751-764(1994).
CC -!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC
CC EMBL; M14273; AAA97414.1;
CC EMBL; A14416; YAA01196.1;
CC EMBL; U16237; AAB60262.1;
CC PIR; A25732; A25732.
CC InterPro: IPR002405; Inhibin_alpha.
CC InterPro: IPR001839; TGFb.
CC Pfam: PF000357; TGF-beta; 1.
CC PRINTS: PR00669; INHIBINA.
CC ProDom: PD000357; TGFb; 1.
CC SMART: SM00204; TGFb; 1.
CC PROSITE: PS00250; TGF-BETA_1; 1.
CC Growth factor; Hormone; Glycoprotein; Signal.
CC SIGNAL 1 17
CC PROPEP 18 226
CC CHAIN 227 360 INHIBIN ALPHA CHAIN.
CC DISULFID 256 322 BY SIMILARITY.
CC DISULFID 285 357 BY SIMILARITY.
CC DISULFID 289 359 BY SIMILARITY.
CC DISULFID 321 321 INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 140 140 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 262 262 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 360 AA; 38809 MW; FBFB385DDIEFEF46 CRC64;
SQ

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Query Match          94.4%; Score 135; DR 1; Length 360;
Best Local Similarity 92.0%; 2nd No. 2.4e-11;
Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1  PWSPALRLLQRPPEPAAHANCHR 25
      IIIIIIIIIIIIIIIIIIIIIIIII
DB      234  PWSPALRLLQRPPEPAAHADCHR 258

RESULT 5
IHA_PIG
ID      IHA_PIG      STANDARD;      PRT;      364 AA.
AC      AC      P04067;
LT      01-NOV-1986 (Rel. 03, Created)
      01-APR-1988 (Rel. 07, Last sequence update)
      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Inhibin alpha chain precursor.
INHA.
QS      SUS scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=86287350; PubMed=3016724;
RA      Mayo K.E., Cerelli G.M., Spless J., Rivier J., Rosenfeld M.G.,
RA      Evans R.M., Vale W.;
RI      "Inhibin A-subunit cDNAs from porcine ovary and human placenta.";
RI      Proc. Natl. Acad. Sci. U.S.A. 83:5849-5853(1986).
RP      [2]
RP      SEQUENCE FROM N.A., AND SEQUENCE OF 231-256.
KC      TISSUE=Ovarian follicular fluid;
RX      MEDLINE=86092207; PubMed=2417121;
RA      Mason A.J., Haylick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
RA      Guillemin R., Niall H., Seeburg P.H.;
RT      "Complementary DNA sequences of ovarian follicular fluid inhibin show
RT      precursor structure and homology with transforming growth
RT      factor-beta.";
RI      Nature 318:659-663(1985).
CC      -|- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC      RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC      INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC      FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC      GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC      ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC      EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC      SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC      ACTIVINS.
CC      -|- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC      INHIBIN A IS A DIMER OF ALPHA AND BETA A.
CC      INHIBIN B IS A DIMER OF ALPHA AND BETA B.
CC      -|- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; M13980; AAA31057.1; -;
CC      FMBI; X03265; CAA27019.1; -;
CC      PIR; A01392; WPGA.
CC      PIR; A25947; A25947.
CC      InterPro; IPR002405; Inhibin_alpha.
CC      InterPro; IPR001839; TGFb.
CC      Pfam; PF00019; TGF_beta; 1.
CC      PRINTS; PR00669; INHIBIN.
CC      ProDom; PD000457; TGFb; 1.
CC      SMART; SM00204; TGFb; 1.
CC      ProSite; PS00250; TGF_BETA_1; 1.
CC      Growth factor; Hormone; Glycoprotein; Signal.

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RP FUNCTION, AND REVIEW.
RX MEDLINE=96321780; PubMed=8701077;
SA Matzuk M.M., Kumar T.R., Shou W., Coerver K.A., Lau A.L.,
RA Behringer R.R., Finegold M.J.;
RT "Transgenic models to study the roles of inhibins and activins in
KL reproduction, oncogenesis, and development.";
CC Recent Prog. Horm. Res. 51:123-154(1996).
CC -!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS. INHIBIN DEFICIENT MICE ARE VIABLE BUT ARE ACUTELY
CC SENSITIVE TO DEVELOPMENT OF GONADAL SEX-CORD STROMAL TUMORS.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
DR FMRL; X69618; CAA49324.1; -.
DR EMBL; M95525; AAA49314.1; -.
DR FMRL; M95526; AAA49314.1; JOINED.
DR EMBL; X55957; CAA39424.1; -.
DR PIR; S31439; S31439.
DR DR; JCI106; JCI106.
DR HSSP; P18075; IIMP.
DR MGI; MGI:96569; Inha.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGPB.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGPB; 1.
DR SMART; SM00204; TGPB; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 233
FT CHAIN 234 366
FT DISULFID 263 328
FT DISULFID 292 363
FT DISULFID 296 365
FT DISULFID 327 327
FT CARBOHYD 147 147
FT CARBOHYD 269 269
FT CONFLICT 165 165
FT CONFLICT 171 171
FT CONFLICT 336 336
SQ SEQUENCE 366 AA; 39536 MW; 8F3851B722FE0011 CRC64;
Query Match 91.6%; Score 131; DB ?; Length 366;
Best Local Similarity 92.0%; Pred. No. 8.6e-11;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 PWSPALRLQLRPPPEAAHANCHR 25
DB 241 PWSPALRLQLRPPPEAAHANCHR 265
|||||:|||||:|||||:|||||:|||||
RESULT 7
ID IHA_RAT
AC P17490; STANDARD; PRT; 366 AA.

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DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inhibin alpha chain precursor.
GN INHA
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurimorphi; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
PC SEQUENCE FROM N.A.
PC TISSUE=Liver;
RX MEDLINE=90190649; PubMed=2628729;
RA Feng Z.-M., Li Y.-P., Chen C.-L.C.;
RT "Analysis of the 5'-flanking regions of rat inhibin alpha- and
RT beta-B-subunit genes suggests two different regulatory mechanisms.";
RL Mol. Endocrinol. 3:1914-1925(1989).
RN [2]
PC SEQUENCE FROM N.A.
RX MEDLINE=91042598; PubMed=3153478;
RA Woodruff T.K., Weinier H., Jones P.B.C., Hsueh A.J.W., Mayo K.E.;
RT "Rat inhibin: molecular cloning of alpha- and beta-subunit
RT complementary deoxyribonucleic acids and expression in the ovary.";
RL Mol. Endocrinol. 1:561-568(1987).
RN [3]
PC SEQUENCE FROM N.A.
RX MEDLINE=90331931; PubMed=2484214;
RA Esch F.S., Shimazaki S., Cocksey K., Mercado M., Mason A.J.,
RA Ying S.Y., Ueno N., Liu N.;
RT "Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence
RT analysis of rat ovarian inhibins.";
RL Mol. Endocrinol. 1:388-396(1987).
RN [4]
PC TISSUE SPECIFICITY.
RX MEDLINE=88124801; PubMed=2826170;
RA Weinier H., Rivier C., Evans R.W., Vale W.;
RT "Gonadal and extragonadal expression of inhibin alpha, beta A, and
RT beta B subunits in various tissues predicts diverse functions.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:247-251(1988).
CC -!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN OVARY AND TESTIS. ALPHA-
CC AND BETA-B-SUBUNITS ARE THE PREDOMINANT FORMS FOUND IN TESTIS.
CC ALSO FOUND IN PLACENTA, PITUITARY, ADRENAL GLAND, BONE MARROW,
CC KIDNEY, SPINAL CHORD AND BRAIN.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
DR EMBL; M32755; AAA41437.1; -.
DR EMBL; M32754; AAA41437.1; JOINED.
DR EMBL; M36453; AAA41435.1; -.
DR PIR; A40905; A40905.
DR PIR; A41398; A41398.
DR PIR; A40056; A40056.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGPB.

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DR Pfam: PF00019; TGF-beta: 1.
DR PRINTS: PR00669; INHIBIN.
DR PRODOM: PD00357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA.1: 1.
KW Growth factor; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 233
FT CHAIN 234 366 INHIBIN ALPHA CHAIN.
FT DISULFID 263 328 BY SIMILARITY.
FT DISULFID 292 363 BY SIMILARITY.
FT DISULFID 296 365 BY SIMILARITY.
FT DISULFID 327 327 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 259 269 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 366 AA; 39496 MW; 327A233B9FEFDCD CRC64;

Query Match 89.5%; Score 128; DB 1; Length 366;
Best Local Similarity 88.0%; Pred. No. 2.2e-10;
Matches 22; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PWSPSALRLRLQRPPEPAHAHANCHR 25
    ||||| ||||| ||||| ||||| |||||
DB 241 PWSPAALRLRLQRPPEPSAHAFCHR 265

RESULT 8
ID IHA_TRIVU STANDARD: PRT; 361 AA.
AC 077755;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin alpha chain precursor.
GN INHA.
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Biprotodontia; Phalangeridae; Trichosurus.
CX NCBI_TaxID:9337;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:99027340; PubMed:9801457;
RA Vamontfort D., Fidler A.E., Heath B.A., Lawrence S.B., Tisdall D.J.,
RA Greenwood P.J., McNatty K.;
RT "cDNA sequence analysis, gene expression and protein localisation of
RT the inhibin alpha subunit of Australian brushtail possum (Trichosurus
RT vulpecula).";
RL J. Mol. Endocrinol. 21:141-152(1998).
CC -!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC RESPECTIVELY. THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF033340; AAC63945.1;
CC InterPro: IPR002405; Inhibin_alpha.
CC InterPro: IPR001839; TGFb.

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DR Pfam: PF00019; TGF-beta: 1.
DR PRINTS: PR00669; INHIBIN.
DR PRODOM: PD00357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA.1: 1.
KW Growth factor; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 230
FT CHAIN 231 361 INHIBIN ALPHA CHAIN.
FT DISULFID 260 323 BY SIMILARITY.
FT DISULFID 289 358 BY SIMILARITY.
FT DISULFID 293 360 BY SIMILARITY.
FT DISULFID 322 322 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 48 48 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 361 AA; 38945 MW; D661CDF93CDAAB7D CRC64;

Query Match 86.7%; Score 124; DB 1; Length 361;
Best Local Similarity 84.0%; Pred. No. 7.7e-10;
Matches 21; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PWSPSALRLRLQRPPEPAHAHANCHR 25
    ||||| ||||| ||||| ||||| |||||
DB 238 PWSPAALRLRLQRPPEPAHADCHR 262

RESULT 9
ID IHA_CHICK STANDARD: PRT; 329 AA.
AC P43031; Q90708;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin alpha chain precursor.
GN INHA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID:9031;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-White leghorn; TISSUE-Ovarian granulosa;
RX MEDLINE=94002740; PubMed=8399835;
RA Wang S.Y., Johnson P.A.;
RT "Complementary deoxyribonucleic acid cloning and sequence analysis of
RT the alpha-subunit of inhibin from chicken ovarian granulosa cells.";
RL Biol. Reprod. 49:453-459(1993).
RN [2]
RP REVISIONS.
RC STRAIN-White leghorn;
RC Johnson P.A., Chen C.C.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.
CC RESPECTIVELY. THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
CC EMBL: AF033340; AAC63945.1;
CC InterPro: IPR002405; Inhibin_alpha.
CC InterPro: IPR001839; TGFb.

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CC -----
 DR EMBL: U48438; AAA92569.1; -.
 DR HSSP: P18075; IBMF.
 DR InterPro: IPR002405; Inhibin_alpha.
 DR InterPro: IPR001839; TGFb.
 DR Pfam: PF00019; TGF-beta; 1.
 DR PRINTS: PR00669; INHIBINA.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFB; 1.
 DR PROSITE: PS00250; TGF_BETA.1; 1.
 KW Growth factor; Hormone; Glycoprotein; Signal.
 FT SIGNAL 1 16 POTENTIAL.
 FT PROPEP 17 216 POTENTIAL.
 FT CHAIN 217 329 INHIBIN ALPHA CHAIN.
 FT DISULFID 242 291 BY SIMILARITY.
 FT DISULFID 271 326 BY SIMILARITY.
 FT DISULFID 275 328 BY SIMILARITY.
 FT DISULFID 290 290 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 248 248 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 329 AA; 35853 MW; AE331687109A25A1 CRC64;

Query Match 71.3%; Score 102; DB 1; Length 329;

Best Local Similarity 72.0%; Pred. No. 7.2e-07;

Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 PWSPSALRLQRPPEPAHANCHR 25

DB 220 PWSPAALSLQLRPSEVAHNCRR 244

RESULT 10

ID GP62_HUMAN STANDARD; PRT; 368 AA.
 AC Q98ZJ7;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable G protein-coupled receptor GPR62.
 GN GPR62
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21105913; PubMed=11165367;
 RA Lee D.K., George S.R., Cheng K., Nguyen T., Liu Y., Brown M.,
 RA Lynch K.R., O'Dowd B.F.;
 RT "Identification of four novel human G protein-coupled receptors
 expressed in the brain."
 RL Brain Res. Mol. Brain Res. 86:13-22(2001).
 CC -!- FUNCTION: Orphan receptor.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in brain; detected in the basal
 CC forebrain, frontal cortex, caudate, putamen, thalamus and
 CC hippocampus.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL: AF317653; AAK12638.1; -.

CC Genew: HGNC:13301; GPR62.

CC MIM: 606917; -

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_REC_F1_1; FALSE_NEG.
 DR PROSITE: PS50262; G_PROTEIN_REC_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 DOMAIN 1 18 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 19 39 1 (POTENTIAL).
 FT DOMAIN 40 53 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 54 74 2 (POTENTIAL).
 FT DOMAIN 75 91 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 92 112 3 (POTENTIAL).
 FT DOMAIN 113 129 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 130 150 4 (POTENTIAL).
 FT DOMAIN 151 177 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 178 198 5 (POTENTIAL).
 FT DOMAIN 199 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 260 6 (POTENTIAL).
 FT DOMAIN 261 272 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 273 293 7 (POTENTIAL).
 FT DOMAIN 294 368 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 239 285 ALA-RICH.
 FT CARBOHYD 3 3 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 8 8 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 368 AA; 37628 MW; 9CFF95298D:2C75 CRC64;

Query Match 38.8%; Score 55.5; DB 1; Length 368;

Best Local Similarity 66.7%; Pred. No. 1.9;

Matches 12; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 2 WSPSA-LRLQLRPPEPA 18

DB 321 WHPRALQLQLRPPEGPA 338

RESULT 11

ID TPO_CANFA STANDARD; PRT; 352 AA.
 AC P42705;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thrombopoietin precursor (Megakaryocyte colony stimulating factor)
 DE (C-MPL ligand) (ML) (Megakaryocyte growth and development factor)
 DE (MGDF).
 GN TPO OR TPO.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-44.
 RC TISSUE=Kidney;
 RX MEDLINE=94291201; PubMed=8020099;
 RA Bartley T.D., Bogenberger J., Hunt P., Li Y.-S., Lu H.S., Martin P.,
 RA Chang M.-S., Samal B.B., Nichol J.L., Swift S., Johnson M.J.,
 RA Hsu R.-Y., Parker V.P., Suggs S., Skrine J.D., Merewether L.A.,
 RA Clogson C., Hsu E., Hokom M.M., Hornkohl A., Choi E., Pangelinan M.,
 RA Sun Y., War V., McNich J., Simonet L., Jacobsen F., Xie C.,
 RA Shutter J., Chute H., Basu R., Selander L., Trollinger D., Sieu L.,
 RA Padilla D., Trail G., Elliott G., Izumi R., Covey T., Crouse J.,
 RA Garcia A., Xu W., del Castillo J., Biron J., Cole S., Hu M.C.-T.,
 RA Pacifici R., Ponting I., Saris C., Wen D., Yung Y.P., Lin H.,
 RA Bosselman R.A.;
 RT "Identification and cloning of a megakaryocyte growth and development
 RT factor that is a ligand for the cytokine receptor Mpl."
 RL Cell 77:1117-1117(1994).
 CC -!- FUNCTION: LINEAGE-SPECIFIC CYTOKINE AFFECTING THE PROLIFERATION
 CC AND MATURATION OF MEGAKARYOCYTES FROM THEIR COMMITTED PROGENITOR
 CC CELLS. IT ACTS AT A LATE STAGE OF MEGAKARYOCYTE DEVELOPMENT. IT
 CC MAY BE THE MAJOR PHYSIOLOGICAL REGULATOR OF CIRCULATING PLATELETS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: TWO-DOMAIN STRUCTURE WITH AN ERYTHROPOIETIN-LIKE N-
 CC TERMINAL AND A SER/PRO/THR-RICH C-TERMINAL.

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CC -!- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
DR InterPro: IPR001323; EPO_TPO.
DR InterPro: IPR003978; thrombopoietin.
DR Pfam: PF00758; EPO_TPO; 1.
DR PRINTS: PR01485; THROMBOPTIN.
DR PROSITE: PS00817; EPO_TPO; 1.
KW Cytokine; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 23
FT CHAIN 24 352 THROMBOPOIETIN.
FT DISULFID 28 172 POTENTIAL.
FT DISULFID 50 106 POTENTIAL.
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 352 AA; 37641 MW; 024F3B41B061FBD8 CRC64;

Query Match 37.1%; Score 53; DB 1; Length 352;
Best Local Similarity 50.0%; Pred. No. 4;
Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 PWSPSALRLQLRPPEPAHAN 22
Db 311 PWSPTQNPQLQPPDPSTAN 332

RESULT 12
NIFZ_FRAAL STANDARD; PRT; 192 AA.
AC P46040;
DT 01-NOV-1995 (Rel. 32, Created)
DE 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE Nifz protein.
GN NIFZ.
OS Frankia alni.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Frankineae; Frankiaceae; Frankia.
OX NCBI_TaxID=1859;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=Cp11;
RX MEDLINE=95369734; PubMed=7642138;
RA Harriott O.T., Hosted T.J., Benson D.R.;
RT "Sequences of nifW, nifX, nifZ, nifB and two ORF in the Frankia
nitrogen fixation gene cluster."
RL Gene 161:63-67(1995).
CC -!- FUNCTION: UNKNOWN.
CC -!- SIMILARITY: BELONGS TO THE NIFZ FAMILY.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L29299; AAC82974.1; -
DR Nitrogen fixation.
SQ SEQUENCE 192 AA; 19002 MW; F226C72F59F50H7A CRC64;

Query Match 35.0%; Score 50; DB 1; Length 192;
Best Local Similarity 31.4%; Pred. No. 5.4;
Matches 11; Conservative 6; Mismatches 4; Indels 14; Gaps 1;

QY 3 SPSSALRLQLRPPEPAHAN-----ANC 23
Db 102 ARAAVLVAKVPAEPAAHGAGGAATCKHOSANC 136

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RESULT 13
DRTS_DAUCA STANDARD; PRT; 528 AA.
AC P45350;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Bifunctional dihydrofolate reductase-thymidylate synthase (DHFR-TS)
DE [Includes: Dihydrofolate reductase (EC 1.5.1.3); Thymidylate synthase
(EC 2.1.1.45)].
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eustetids II; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lunga di Amsterdam;
RX MEDLINE=93320381; PubMed=8329682;
RA Luo M., Piffaneil P., Kestell L., Cella R.;
RT "Molecular cloning and analysis of a cDNA coding for the bifunctional
dihydrofolate reductase-thymidylate synthase of Daucus carota."
RL Plant Mol. Biol. 22:427-435(1993).
CC -!- CATALYTIC ACTIVITY: 5,6,7,8-tetrahydrofolate + NADP(+) -> 7,8-
dihydrofolate + NADPH.
CC -!- CATALYTIC ACTIVITY: 5,10-methyl tetrahydrofolate + dUMP ->
dihydrofolate + dTMP.
CC -!- PATHWAY: ESSENTIAL STEP FOR DE NOVO GLYCINE AND PURINE SYNTHESIS,
DNA PRECURSOR SYNTHESIS, AND FOR THE CONVERSION OF DUMP TO dTMP.
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
DIHYDROFOLATE REDUCTASE FAMILY.
CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE THYMIDYLATE
SYNTHASE FAMILY.
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CC -----
DR EMBL; Z17306; CRA78954.1; -
DR HSSP; P45352; DRTS.
DR InterPro: IPR001796; DHFR.
DR InterPro: IPR000398; Thymidylat_synt.
DR Pfam; PR00186; Dihfolate_red; 1.
DR Pfam; PR00303; thymidylat_synt; 1.
DR PRINTS; PR00070; DHFR.
DR PRINTS; PR00108; THYMIDYLAT_SYNTH.
DR PRODOM; PD001180; Thymidylat_synt; 1.
DR PROSITE; PS00075; DHFR; 1.
DR PROSITE; PS00091; THYMIDYLATE_SYNTHASE; 1.
KW Multifunctional enzyme; oxidoreductase; Transferase; NADP;
Methyltransferase; Nucleotide biosynthesis; One-carbon metabolism.
FT DOMAIN 1 201 DIHYDROFOLATE REDUCTASE.
FT DOMAIN 202 528 THYMIDYLATE SYNTHASE.
FT ACT_SITE 409 409 BY SIMILARITY.
SQ SEQUENCE 528 AA; 59258 MW; 8BE07C221A546A56 CRC64;

Query Match 35.0%; Score 50; DB 1; Length 528;
Best Local Similarity 43.5%; Pred. No. 16;
Matches 10; Conservative 2; Mismatches 3; Indels 8; Gaps 1;

QY 2 WSPSALRLQLRPPEPAHAN 24
Db 396 WNPSDLRLMALPP-----CH 410

RESULT 14
SM6B_HUMAN STANDARD; PRT; 888 AA.
ID SM6B_HUMAN

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AC Q9H3T3; Q9NRK9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Semaphorin 6B precursor (Semaphorin Z) (Sema Z).
 GN SEMA6B OR SEMA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RA Kimura T., Ishida H.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=21245680; PubMed=11350127;
 RA Correa R.G., Sushara R.M., Bengtson M.H., Katayama M.L.H.,
 RA Salim A.C.M., Brentani M.M., Sogayar M.C., de Souza S.J.,
 RA Simpson A.J.G.;
 RT "Human semaphorin 6b";
 RL Genomics 73:343-348(2001).
 CC -!- FUNCTION: MAY PLAY A ROLE IN BOTH PERIPHERAL AND CENTRAL NERVOUS
 CC SYSTEM DEVELOPMENT (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: At least 2 isoforms; 1 (shown here) and
 CC 2/6B.1; are produced by alternative splicing.
 CC -!- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
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 DR EMBL; AB022433; BAB20669.1; -;
 DR EMBL; AF216389; AAF87661.1; -;
 DR Genew; HGNC:10739; SEMA6B.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00286; PTI; 1.
 DR Signal; Transmembrane; Multiqene family; Neurogenesis; Glycoprotein;
 KW Developmental protein; Alternative splicing.
 FT SIGNAL 1 25
 FT CHAIN 26 888
 FT DOMAIN 26 603
 FT TRANSMEM 604 624
 FT DOMAIN 625 888
 FT DOMAIN 238 547
 FT DOMAIN 561 674
 FT DOMAIN 750 753
 FT CARBOHYD 74 74
 FT CARBOHYD 155 155
 FT CARBOHYD 167 167
 FT CARBOHYD 291 291
 FT CARBOHYD 386 386
 FT CARBOHYD 441 441
 FT CARBOHYD 462 462
 FT VARSPLIC 471 517
 AAFFRC -> RVCQVGHACVCHVRRSWPQRPGRWLSRR
 LSVELEEFETYPDRGCRGGGTGQRLLSLELDAASGGILL
 MISSING (IN ISOFORM 2).
 D -> E (IN REF. 2).
 FT VARSPLIC 518 888
 FT CONFLICT 30 30
 FT SEQUENCE 888 AA; 95270 MW; 6FFB44D682BC70CB CRC64;
 Query Match 33.9%; Score 48.5; DB 1; Length 888;

Best Local Similarity 28.9%; Pred. No. 43;
 Matches 13; Conservative 1; Mismatches 10; Indels 21; Gaps 2;
 QY 1 PWSPSALRLRLQRP--PEPPAA-----HANCH 24
 DB 820 PWSPPPTGSLRRPLGPHAPPATLRTTHIFNSGARGGKRGSC 864
 RESULT 15
 HMID_DROAN
 ID HMID_DROAN STANDARD; PRI; 606 AA.
 AC P22544;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Homeobox protein OM(1D).
 GN OM(1D).
 OS Drosophila ananassae (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7217;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91122048; PubMed=1671353;
 RA Tanda S., Corcos V.G.;
 RT "Retrosposon-induced overexpression of a homeobox gene causes
 RT defects in eye morphogenesis in Drosophila";
 RL EMBO J. 10:407-417(1991).
 CC -!- FUNCTION: Probably involved in eye morphogenesis.
 CC -!- SUBCELLULAR LOCATION: Nucleus (Potential).
 CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
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 DR EMBL; X56682; CAA40011.1; -;
 DR PIR; S13367; S13367.
 DR HSP; P14653; I872.
 DR TRANSFAC; T03732; -;
 DR FlyBase; FBgn0012114; DanaX.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; H-MEBOX.
 DR ProDom; PD000016; Homeobox; 1
 DR SMART; SM00384; HOX; 1.
 DR PROSITE; PS00027; Homeobox-X_1; 1.
 DR PROSITE; PS50071; Homeobox_2; 1.
 KW DNA-binding; Homeobox; Developmental protein; Nuclear protein; Vision.
 FT DOMAIN 23 57 HIS/GLN-RICH (OPA-REPEAT).
 FT DOMAIN 106 124 HIS/PRO-RICH.
 FT DOMAIN 173 193 HOMEBOX.
 FT DOMAIN 220 248 ALA-RICH.
 FT DOMAIN 422 434 ALA-RICH.
 FT DOMAIN 450 455 ALA-RICH.
 FT DOMAIN 503 510 ALA-RICH.
 FT DOMAIN 515 521 PRO-RICH.
 SQ SEQUENCE 606 AA; 61735 MW; AA7BB6367370FBB CRC64;
 Query Match 33.6%; Score 48; DB 1; Length 606;
 Best Local Similarity 56.2%; Pred. No. 34;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 9 LIQRPPEPPAAHANCH 24
 DB 8 LTQTPSETPAHSQLH 23

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Job time : 15 secs